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Title:
Perfect score:
Sequence:
                                                                                                                                                                          Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8:
                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                             1005.5
965.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB DB
                               778.5
778.5
185
160.5
159.5
159.5
159.5
159.5
                                                                                                                         851
846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq
seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                                   10:
11:
12:
13:
14:
15:
16:
17:
  84.2
80.9
70.3
77.3
65.2
65.2
113.4
113.4
113.3
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113.6
111.8
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maximum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562222 seqs, 172994929 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    August 28, 2002, 17:31:09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPPNLPDPKFESKAALLAA.......GGFWSAWSEPVSLLTPSDLD
                                                                                                                                                                                                                                                                        sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                     sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                        sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                            sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                           sp_fungi:*
                                                                                                                                                                                                                                                                                                                                               sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                     sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                   sp_human:*
                                                                                                                                                                                                                                                                  sp_archeap:*
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                                                                                                                                                                          Length DB
  509
2299
2299
289
316
418
561
422
422
422
422
296
626
627
6227
                                                                                                                                                                                                                                                                                                                                                                                                                                                             first
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   Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100%
 Q9UHH5
018880
1 Q9JM58
046561
9 Q90WG7
Q9GLW3
Q9XS92
Q9NOJ7
                                                                                Q9MYZ9
035545
Q27950
Q28206
Q28206
Q95N13
Q95N14
L Q925F5
075462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search time 63.43 Seconds (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613.651 Million cell updates/sec
                                      Q9myz9 sus scrofa
035545 rattus norv
027950 bos indicus
028206 bos taurus
028206 bos taurus
095n13 ovis aries
095n14 ovis aries
092515 mus musculu
075462 homo sapien
018880 bos taurus
09jm58 mus musculu
045561 ovis aries
Q90wg7 cynops pyrr
Q9g1w3 ursus marit
Q9xs92 trichosurus
Q9n0j7 callithrix
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106.5	107.5	108.5	110.5	111.5 $111$	112.5 $111.5$	113.5	114.5	118.5	122	122	123.5	123.5	126	126	128	128	128
	9.00			9 . 3 3	9.4	9.5	9.6		•		10.3		•	10.6	10.7	10.7	10.7
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Q14213 Q14217 Q9UEH7	Q9JKT1 Q9JKG1	Q63216 Q9DE35	Q95ML5 Q9PTPO	Q9PTI0 018985	Q9TU69 Q9IBF6	Q9UB28	Q9N0Y7	Q9DFU0	093404	Q16354	070535	Q90Z16	Q99JZ1	Q96TF0	Q96P35	д9инл5	Q96P36
Q14213 homo sapien Q9ueh7 homo sapien	Q9jktl cavia porce Q9jkgl cavia porce Q9jig7 cavia porce		Q95ml5 saimiri bol Q9ptp0 carassius a	xenopus ervus el	Q9tu69 canis famil Q9ibf6 xenopus lae	Q9ub28 caenorhabdi	Q9nOy7 monodelphis O9ub29 caenorhabdi	Q9dfuO sparus aura	093404 oreochromis			paralic	Q99jzl mus musculu	OMO	homo	homo	Q96p36 homo sapien

## ALIGNMENTS

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RESULT
QPMYZ9
ID VZ9
AC Q9
AC Q9
DT Q1
DT 
"Porcine Erythropoietin Receptor: Molecular Cloning and Expression in Tembryonic and Fetal Liver.";
Domest. Anim. Endocrinol. 0.0-0(2000).

EMBL; AF274305; AAF77065.1; -.

REMBL; AF274305; ENEMATTORES.1; -.

REMBL; AF274305; ALF77065.1; -.

REMBL; ALF74305; ALF74305; ALF77065.1; -.

REMBL; ALF74305; ALF7430
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Q9MYZ9;
Q1-OCT-2000 (TrEMBLrel. 15,
Q1-OCT-2000 (TrEMBLrel. 15,
Q1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pearson P.L., Smith T.P.L., So Christenson R.K., Vallet J.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissue=Liver;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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RESULT
Q27950
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ODS 545

ODS 645

ODS 
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Best Local S
Matches 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyatake
"The intr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98296111; PubMed-9630610;
MEDLINE-98296111; PubMed-9630610;
Mirakami C., Takenoshita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TREMBLrel. 05, Created)
01-JAN-1998 (TREMBLrel. 19, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
INTRON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR PI
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Receptor.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed as a membrane-bound form.";
Biochim. Biophys. Acta 1403:169-178(1998).
EMBL; D83509; BAA22373.1; -.
HSSP; P19235; 1EBA.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                               204
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                                                                              CVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPS
                                                                                                                                           LDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE
                                                                                                                                                                                                          DEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHINEVVL
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                                                                                                                                                                                        GESRKSCRLHQAPTVRGSMRFWCSLPTADTSSFVPLELQVTEASGSPRYHRIIHINEVVL
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                                                                                                                            LDAPAGLLARRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTE
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316 i
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316
34220
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Pred. No. 5.
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5.2e-83;
hes 23;
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Matches 161
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Q28206;
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NON_TER
SEQUENCE
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TISSUE-BONE MARROW;
Suliman H.B., Feldman B.F., M
Submitted (JUN-1996) to the E
EMBL; U61398; AAB03870.1; -.
HSSP; P19235; 1EBA.
InterPro; IPR002996; CRIA.
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Q27950;
Q1-NOV-1996 (TrE
01-NOV-1996 (TrE
01-DEC-2001 (TrE
ERYTHROPOIETIN F
TISSUE-BONE MARROW;
Suliman H.B., Feldman B.F.,
Submitted (JUN-1996) to the
EMBL; U61399; AAB03871.1; -.
HSSP; P19235; 1EBA.
                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
ERYTHROPOIETIN RECEPTOR
                                                                                                                           BOS taurus (Bovine)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                         SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=9913;
                                                                                                                  Bovidae; Bovinae;
                                                                                                                                                                                                                                    01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos indicus
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                                                                                                                                                                                                                                                                                                                                        PASLLTASDLD
                                                                                                                                                                                                                                                                                                                                                                   PVSLLTPSDLD
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                                                                                                                   Bos.
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25196
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                                                                                                                                 Cetartiodactyla;
                                                                                                                                              Chordata;
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Hematopo_receptor_L_F1.
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Last sequence up
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EMBL/GenBank/DDBJ
                              Majiwa P.A.O., Logan-Henfrey EMBL/GenBank/DDBJ databases.
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                                                                                                                               Craniata; Vertebrat
actyla; Ruminantia;
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                                                                                                                                 Vertebrata; Euteleostomi;
minantia; Pecora; Bovoidea
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)BJ databases.
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Best Local :
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Q95N13;
Q1-DEC-2001 (TrEMBLrel. 19, Crea
O1-DEC-2001 (TrEMBLrel. 19, Last
O1-DEC-2001 (TrEMBLrel. 19, Last
ERYTHROPOISTIN RECEPTOR (FRAGME)
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; C:
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SEQUENCE
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NCBI_TaxID=9940;
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                                                                                                                                                                                                   Submitted (APR-2001) to the EMBL; AY029232; AAK38737.1;
                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Cetartiodactyla;
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                          -SGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSA
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                                                                    ATAGVGPDNYSFSYQLEGEPWKPCRLHQTPTARGLVRFWCSLPTADTSSFVPLELHVTAA
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IPR003961; FN_III.
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Pred.
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red. No. 2.8e
Mismatches
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2.8e-65;
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Best Local Similarity
                                                         SEQUENCE FROM Sabath D.F., L Broudy V.C.;
                                                                                                                                                                                                                                                                                                                     Q925F5;
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SEQUENCE
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"Identification and characterization of an isc
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AF360122; AAK52492.1; -.
                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                                                                                                                                                                       C-MPL-II.
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2001) to the EMBL; AY029231; AAK38170.1;
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the ovine fetus.";
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Bovidae; Caprinae; C
NCBI_TaxID=9940;
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Lofton-Day
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Rodentia;
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82.0%;
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Last sequence user that annotation
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Pred. No. 3.1
                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
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075462;
01-NOV-1998
                                                                                                                                                                                                                                                         Signal;
SIGNAL
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YYu...
Yarina (Human).
Homo sapiens (Human).
Homo sapiens (Human).
Horia; Metazoa; Chordata;
Horia; Primates;
                                                                                                                                                                                                                                                                                     InterPro; irnver
InterPro; IPR003961; FN.
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AF059293; AAC28335.1; -. EMBL; AF073515; AAD39681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                Magrangeas F., Jacques Y., Minvielle S.;
"Cloning and expression of a novel soluble hematopoietic cytokine receptor domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYTOKINE-LIKE FACTOR-1 PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002996; CR1A.
                                                          138
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                                                                                        PEELLCFTERLEDLVCFWEEAASAGVGPG-----NYSFSYQLEDEPW----KLCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD
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                    HQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS--GAPRYH-RVIHINEVVLLDAPVG
                                                      PVNISCWSKNMKDLTCRWT-----PGAHGETFLHTNYSLKYKLR---WYGQDNTCEE
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422 AA;
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46301 MW;
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27.0%;
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                                                                                                                           Score 160.5;
Pred. No. 5.8e
29; Mismatches
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CYTOKINE-LIKE FACTOR-1
AD9DEFCB01B84228 CRC
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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
              Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lok S., Presnell S.R., Jelmberg A.C., Gilbert T., Whitmc Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF178684; AAD54385.1; -.
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Pfam; PF00041; fn3; 
SMART; SM00060; FN3;
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Mammalia; Eutheria;
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Bovidae; Bovinae; Bos
                                                                          PROLACTIN RECEPTOR SHORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 PEELLCFTERLEDLVCFWEEAASAGVGPG------NYSFSYQLEDEPW----KLCRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRLAGLKPGTVYFVQVRCN----PFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVLSNLRGRTRYTFAVRARMAEPSFG-----GFWSAWSEPVSLLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YHTVGPHS-----CHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                      CRLAGLKPGTVYFVQVRCN----PFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSV-----DWKVVDDVSNQTS
                                                                                                                                                                                                                                                                                                                                                                  L-VARLADESGHVVLRWLPPPET-----PMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 180 : |:|: : :| :| : :|
                                                                                                                                                                                                                                                                                                                                                                                                                          YHTVGPHS-----CHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS--GAPRYH-RVIHINEVVLLDAPVG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVNISCWSKNMKDLTCRWT-----PGAHGETFLHTNYSLKYKLR---WYGQDNTCEE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSV-----DWKVVDDVSNQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-VARLADESGHVVLRWLPPPET-----PMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P16471; 1BP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002996; CR1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                          PRELIMINARY;
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2.
                    Chordata; Crania
Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46315 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13,
13,
                                                                                          05, Created)05, Last sequence update)19, Last annotation updat
                                                                              FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 159.5; I
Pred. No. 7.3e
29; Mismatches
                Craniata; Vertebrat
actyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                            296
                                    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3e-07;
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                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                      Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422;
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Best Local S
Matches 55
  Best Loc
Matches
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JM58;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Hiroyama T., Iwama A., Nakamura Y., Hiroyama T., Iwama A., Nakamura Y., "Cytokine receptor like molecule 3." Submitted (MAR-2000) to the EMBL/Geni EMBL; AB040038; BAA92777.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOKINE RECEPTOR LIKE CRLF1 OR CRLM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrembLrel. 01-OCT-2000 (TrembLrel. 01-DEC-2001 (TrembLrel.
                                                                                                                                                                                                                                                  MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endocrinology 138:3187-3194(1997).
EMBL; AF027403; AAB83999.1; -.
HSSP; P14787; 1AN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-97375450; PubMed-9231767;
Schuler L.A., Nagel R.J., Gao J.,
"Prolactin receptor heterogeneity
                                                                                                                          Signal; Receptor.
SIGNAL 1
                                                                                                                                                                                 InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_IIII
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
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                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLAARGPEE----LLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:1340030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFIIQYEIRLKPEKATDWETHFTLKQ--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLKIFNLYPGQKYLVQIRCK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLVARL---ADESGHVVLRWLPPPETPMTSH---IRYEVDVSAGNGAGSVQRVEILEGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPDYKTGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLY---VHVTYIVEPEPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APTARGAVREWCSLPTADTSSEVPLELRVTA-----ASGAPRYHRVIHINEVVLLDAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLLNGQSPPEKPKLVKCRSPGKETFTCWWEPGADGGL-PTNYTLTYHKEGE----TLIHE
                                                                                                                                                                                                                                                                   P16471; 1BP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
                                                                                                       425 AA;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AΑ;
                                                                                                                                                                                                                                                Crlf1
                                                                                                     34
46662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              `, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33854 MW;
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                       13
25
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Hematopo_receptor_L_F1.
                       . 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE 3 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15, Created)15, Last sequence update)19, Last annotation updat
    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PDH-GYWSEWSPESSIQIPND
Score 157.5;
Pred. No. 1.1e
29; Mismatches
                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                                                                                 POTENTIAL.
; 910535C629CA7056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 159;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9F1C15FB41DE0787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horseman N.D., in bovine fetal
                                                                                                                                                                                                                                                                                                                                               Nakauchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425
                       .1e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
    85
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kessler M.A.;
l and maternal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                        Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae;
  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189
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  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (L
PITUITARY, ADRENAL GIAND, OVARY AND FETAL LIVER).
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
EMBL; AF04197; AAB96795.1; -.
EMBL; AF04197; AAB968920.1; -.
EMBL; AF04197; AAB97082.1; -.
EMBL; AF042358; AAB97744.1; -.
EMBL; AF042358; AAB97743.1; -.
EMBL; AF041978; AAB96955.1; -.
EMBL; AF041978; AAB96955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             046561 PRELIMINARY; 581 AA. 046561; P79205; 046574; 046573; P79203; 046569; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat PROLACTIN RECEPTOR PRECURSOR (PRL-R) (PRLR) (OPR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane and Short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents.";

J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                          -i- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- ALTERNATIVE PRODUCTS: THREE ISOFORMS; LONG ISOFORM
                                                                                                                                                                                                                                                                                                            Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F., "Two forms of the prolactin receptor messenger ribonucleic present in ovine fetal liver and adult ovary.";
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 147-302 FROM N.A., AND ALTERNATIVE TISSUE=FETAL LIVER, AND CORPUS LUTEUM;
                                                                                                                                                                                                                                                                                                                                                                                                                  "Detection of prolactin receptor gene expression i pituitary gland and visualization of the specific signal in gonadotrophs.";
Endocrinology 139:5215-5223(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN-SCOTTISH BLACKFACE / ISOLATE M22/80; TISSUE-ANTERIOR PITUITARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
Bovidae; Caprinae; (
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                            -i- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PROLACTIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                               Endocrine 3:291-295(1995).
                                                                                                                                                                                                                                                                                                                                                                TISSUE=FETAL LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tortonese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99049302; PubMed=9832462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98001468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-MAMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
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                                                                                                                                                                                         ALTERNATIVE SPLICING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS
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                                                                                                                                                                                                          SHORT ISOFORM (S-OPR) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLAND, AND LIVER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND ALTERNATIVE SPLICING
                                                                                                                                                                                                           SOLUBLE
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c translation
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                                                                                                                                                                                                                                                                              PITUITARY
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VARSPLIC
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                                                                                                                                                                                                                                    Q90WG7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
PROLACTIN RECEPTOR PRECURSOR.
Yamamoto.T., Nakayama Y., Matsuda Y., Abe S.-I.; "Cloning and expression of a cDNA encoding a prolactin Japanese red-beliled newt, Cynops pyrrhogaster."; Zool. Sci. 15:741-747(1998).
                                                                                                                                                                        Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cyno
                                                                                         TISSUE=KIDNEY;
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  Q90WG7
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                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAPTARGAVRFWCSLPTADTSSFVPLELRVTA-----ASGAPRYHRVIHINEVVLLDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQLKIFNLYPGQKYLVQIRCK---PDH-GYWSEWSPESFIQIPND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNLTLELKHPEDRKPYLWIKWSPPTLTDVKSGWFSIQYEIRLKPEKATD--WETHFAPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGLVARL---ADESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQRVEILEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECPDYKTGGPNSCYFSKKYTSIWKMYVITVSAINQMGISSSDPLY---VDVTYIVEPEPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y10808; CAA71766.1;
P14787; 1AN3.
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IPR003961; FN_III.
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281
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ISOFORM).
MISSING (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 151; DB 6;
Pred. No. 6.8e-06
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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

QOSPPEKPKLIKCRSPCKETFTCWWEDEADGGLPTNYTLTY

RK -> ASLYVPGGKCSSVCTYMAYPFVGGIFLHMYLCVDQ

YLLTYTS (IN SOLUBLE ISOFORM).

MISSING (IN SOLUBLE ISOFORM).
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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V (IN AAB97743 AND AAB97744).

K (IN REF. 2).

EC534FDE538837A0 CRC64;
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Signal; Receptor.
SIGNAL 1
SEQUENCE 626 AA;
                                                                                                                                                                Receptor.
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                            Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M.; "Cloning and sequence analysis of the extracellular region of the polar bear (Ursus maritimus) luteinizing hormone receptor (FSHr), and prolactin receptor (PRLr) genes and their expression in the testis of the black bear
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                            Ursus maritimus (Polar bear) (Thalarctos maritimus) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9GLW3
                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                   SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                (Irsus americanus).";
Mol. Reprod. Dev. 55:136-145(2000).
EMBL; AP169792; AAG10648.1; -.
HSSP; P14787; laN3.
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20086658; PubMed=10618652;
                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=29073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROLACTIN RECEPTOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001
                                                                                                                                                                                                             InterPro; IPRO
Pfam; PF00041;
                                                                                                                                                                                                                                    InterPro;
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                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPSENYIVQVRCK----SDHGFWSMWSPESYIQIPDN 229
TMYIITINATNQMGSSSSDPRY--
                                                         EDLYCFWEEAASAGYGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVVLRWLPPPETPMTS---HIRYEVDVSAGNG-----AGSVQRVEILEGRTECVLSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CFFDKKHTSIWTMYNIIVNATNELGSTTSDPKF----VDVAYIVQLRPPLNVTLSIIYEPP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSLPTADTSSFVPLELRVTA-----ASGAPRYHRVIHINEVVLLDAPVGLVARLADESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVNIMCRSPEKETFSCWWQPGSDGGL-PTNYSLLYKTEGKN----TYSECPDYKTSGPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFW
                    VPLELRVTA-----ASGAPRYHRVIHINEVVLLDAPVGLVARL---ADESGHVVLRWLP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLLVKWSPPSEADVKSGWVTIEYEVQFKSKKAKEWETLTAGKQRQLKVF--
                                              ETFTCWWKPGEDGGL-PTNYTLTYRKEGE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB005045; BAB61107.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                      Similarity
                                                                                                                                                                                                            IPR002996; CR1A.
IPR003961; FN_III
0041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        626 AA;
                                                                                                                                                    227
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                      AA;
                                                                                                                                                    227
26114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata;
Carnivora; Fissipedia; Ursidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 I
69944 MW;
                                                                                                      11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence up
                                                                                        Score 140; DB
Pred. No. 2.3e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
; B6050DD9C9F58DE5 CRC64;
-VDVTYIVEPDPPVNLTLELKQPEDKKPYLWMKWYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                      F5E6C5F33B5D5B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140.5;
No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
                                             -TTTHECPDYISSGPNSCYFNKKHTSIW
                                                                                           DB 6;
2.3e-05;
tes 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3e-05;
es 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                Length
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SL
                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
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                                              56
                                                                      93
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Search completed: August 28, Job time: 546 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The prolactin receptor from the brushtail possum (Trichosurus vulpecula): cDNA cloning, expression and functional analysis."; Mol. Cell. Endocrinol. 148:119-127(1999).

EMBL; AF098296; AAD27039.1; -.

HSSP; P14787; 1AN3.
Interpro; IPR00396; CR1A.
Interpro; IPR00396; FRIII.
Interpro; IPR003981; FM_III.
Interpro; IPR00328; Hematopo_receptor_L_F1.

Pfam; PF00041; fn3; 2.

SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XS92 PRELIMINARY; PRT; 625 AA. Q9XS92; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PROLACTIN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Diprotodontia; Phalangeridae;
NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01352;
Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99236966; PubMed=10221777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 QVRCK---PDH-GFWSEWSPESSIQIPNDV 190
                                                                           187
                                                                                                                                      129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 AVRARMAEPSFGGFWSAWSEPVSLLTPSDL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114
                                                                                                     177 GRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDL 224
                                                                                                                                                               123 APVGL---VARLADESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQRVEILE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 PPETPMTS---HIRYEVDVSAGNG------AGSVQRVEILEGRTECVLSNLRGRTRYTF 194
                                                                                                                                                                                            72 THECPDYKTGGPNSCYFNKKHTSIWMYYIIWVNATNQMGRSMSEPRY---VDVTYIVEPD
                                                                                                                                                                                                                69 LHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS------GAPRYHRVIHINEVVLLD 122
                                                                                                                                                                                                                                                           31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                      PKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCR 68
                                                                        QQTQFKIFSLYLGQKYLVEVRCK---PDHGS-WSQWSPESSILIPSDI 230
                                                                                                                                   PPLNLTLEVKQPEDGKPYLWLKWSPPVLVDVRSGWLTLQYELRLKPEKAA--EWETHFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTLVDVRSGWLTLQYEIRLKPEKATEWETHFAGQQTQFKIL-----SLYPGQKYLV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                25
625 AA;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                           24 POTENTIAL.
625 PROLACTIN RECEPTOR.
70539 MW; 2097D72827C9DBB6 CRC64;
                                                                                                                                                                                                                                                                                                                                 11.6%; Score 139; DB 6; Length 625; 24.6%; Pred. No. 0.0001;
              2002, 17:40:15
                                                                                                                                                                                                                                                                                                                    34; Mismatches
                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Trichosurus.
                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                    186
                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                    11;
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